



RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/964,994

DATE: 01/23/2002
TIME: 09:44:51

Input Set : A:\P3121R1.txt
Output Set: N:\CRF3\01222002\I964994.raw

ENTERED

3 <110> APPLICANT: Goddard,Audrey
4 Godowski,Paul J.
5 Gurney,Austin L.
6 Watanabe,Colin K.
7 Wood,William I.
9 <120> TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING SEQUENCE SIMILARITY TO
10 CYTOKINE RECEPTORS AND NUCLEIC ACIDS ENCODING THE SAME
12 <130> FILE REFERENCE: P3121R1
14 <140> CURRENT APPLICATION NUMBER: US 09/964,994
15 <141> CURRENT FILING DATE: 2001-09-26
17 <150> PRIOR APPLICATION NUMBER: PCT/US00/08439
18 <151> PRIOR FILING DATE: 2000-03-30
20 <150> PRIOR APPLICATION NUMBER: PCT/US01/06520
21 <151> PRIOR FILING DATE: 2001-02-28
23 <150> PRIOR APPLICATION NUMBER: US 60/191,015
24 <151> PRIOR FILING DATE: 2000-03-21
26 <150> PRIOR APPLICATION NUMBER: US 09/941,992
27 <151> PRIOR FILING DATE: 2001-08-28
29 <160> NUMBER OF SEQ ID NOS: 7
31 <210> SEQ ID NO: 1
32 <211> LENGTH: 1318
33 <212> TYPE: DNA
34 <213> ORGANISM: Homo Sapien
36 <400> SEQUENCE: 1
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39 cttcataaga ggattaacaa agacaaaata tgggaaaaac ataacatggc 100
41 gtcccataat tattagatct tattattgac actaaaatgg cattaaaatt 150
43 accaaaagga agacagcatc tgtttcctct ttggtcctga gctggttaaa 200
45 aggaacactg gttgcctgaa cagtcacact tgcaaccatg atgcctaaac 250
47 attgctttct aggcttcctc atcagtttct tccttactgg tgtagcagga 300
49 actcagtcaa cgcatgagtc tctgaagcct cagagggtac aatttcagtc 350
51 ccgaaatttt cacaacattt tgcaatggca gcctgggagg gcacttactg 400
53 gcaacagcag tgtctatttt gtgcagtaca aaatcatgtt ctcatgcagc 450
55 atgaaaagct ctcaccagaa gccaaagtga tgctggcagc acatttcttg 500
57 taacttccca ggctgcagaa cattgggctaa atatggacag agacaatgga 550
59 aaaataaaga agactgttgg ggtactcaag aactctcttg tgaccttacc 600
61 agtgaaacct cagacataca ggaaccttat tacgggaggg tgagggcggc 650
63 ctcggctggg agctactcag aatggagcat gacgccgcgg ttactccct 700
65 ggtgggaaac aaaaatagat cctccagtca tgaatataac ccaagtcaat 750
67 ggctctttgt tggtaattct ccatgctcca aatttaccat atagatacca 800
69 aaaggaaaaa aatgtatcta tagaagatta ctatgaacta ctataccgag 850
71 tttttataat taacaattca ctagaaaagg agcaaaaggt ttatgaaggg 900
73 gctcacagag cggttgaaat tgaagctcta acaccacact ccagctactg 950

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75  tgtagtggct gaaatatatc agcccatggt agacagaaga agtcagagaa 1000
77  gtgaagagag atgtgtggaa attccatgac ttgtggaatt tggcattcag 1050
79  caatgtggaa attctaaagc tccctgagaa caggatgact cgtgtttgaa 1100
81  ggatcttatt taaaattggt tttgtatatt cttaaagcaa tattcactgt 1150
83  tacaccttgg ggacttcttt gtttatccat tcttttatcc tttatatattc 1200
85  atttgtaaac tatatttgaa cgacattccc cccgaaaaat tgaaatgtaa 1250
87  agatgaggca gagaataaag tgttctatga aaaaaaaaaa aaaaaaaaaa 1300
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91 <210> SEQ ID NO: 2
92 <211> LENGTH: 262
93 <212> TYPE: PRT
94 <213> ORGANISM: Homo Sapien
96 <400> SEQUENCE: 2
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100  Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro
101          20          25          30
103  Gln Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln
104          35          40          45
106  Trp Gln Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe
107          50          55          60
109  Val Gln Tyr Lys Ile Met Phe Ser Cys Ser Met Lys Ser Ser His
110          65          70          75
112  Gln Lys Pro Ser Gly Cys Trp Gln His Ile Ser Cys Asn Phe Pro
113          80          85          90
115  Gly Cys Arg Thr Leu Ala Lys Tyr Gly Gln Arg Gln Trp Lys Asn
116          95         100         105
118  Lys Glu Asp Cys Trp Gly Thr Gln Glu Leu Ser Cys Asp Leu Thr
119         110         115         120
121  Ser Glu Thr Ser Asp Ile Gln Glu Pro Tyr Tyr Gly Arg Val Arg
122         125         130         135
124  Ala Ala Ser Ala Gly Ser Tyr Ser Glu Trp Ser Met Thr Pro Arg
125         140         145         150
127  Phe Thr Pro Trp Trp Glu Thr Lys Ile Asp Pro Pro Val Met Asn
128         155         160         165
130  Ile Thr Gln Val Asn Gly Ser Leu Leu Val Ile Leu His Ala Pro
131         170         175         180
133  Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn Val Ser Ile Glu
134         185         190         195
136  Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile Asn Asn Ser
137         200         205         210
139  Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg Ala Val
140         215         220         225
142  Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val Ala
143         230         235         240
145  Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
146         245         250         255
148  Glu Arg Cys Val Glu Ile Pro
149         260

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151 <210> SEQ ID NO: 3
152 <211> LENGTH: 27
153 <212> TYPE: DNA
154 <213> ORGANISM: Artificial Sequence
156 <220> FEATURE:
157 <223> OTHER INFORMATION: Synthetic oligonucleotide probe
159 <400> SEQUENCE: 3
160 ctggcaacag cagtgtctat tttgtgc 27
162 <210> SEQ ID NO: 4
163 <211> LENGTH: 21
164 <212> TYPE: DNA
165 <213> ORGANISM: Artificial Sequence
167 <220> FEATURE:
168 <223> OTHER INFORMATION: Synthetic oligonucleotide probe
170 <400> SEQUENCE: 4
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173 <210> SEQ ID NO: 5
174 <211> LENGTH: 52
175 <212> TYPE: DNA
176 <213> ORGANISM: Artificial Sequence
178 <220> FEATURE:
179 <223> OTHER INFORMATION: Synthetic oligonucleotide probe
181 <400> SEQUENCE: 5
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184 tc 52
186 <210> SEQ ID NO: 6
187 <211> LENGTH: 1705
188 <212> TYPE: DNA
189 <213> ORGANISM: Homo Sapien
191 <400> SEQUENCE: 6
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194 tctgattggt gaatggtgaa ggtgcctgtc taacttttct gtaaaaagaa 100
196 ccagctgcct ccaggcagcc agccctcaag catcacttac aggaccagag 150
198 ggacaagaca tgactgtgat gaggagctgc tttcgccaat ttaacaccaa 200
200 gaagaattga ggctgcttgg gaggaaggcc aggaggaaca cgagactgag 250
202 agatgaattt tcaacagagg ctgcaaagcc tgtggacttt agccagaccc 300
204 ttctgccctc ctttgcctggc gacagcctct caaatgcaga tggttgtgct 350
206 cccttgctg ggtttttacc tgcttctctg gagccaggta tcagggggccc 400
208 agggccaaga attccacttt gggccctgcc aagtgaaggg ggttggtccc 450
210 cagaaactgt ggggaagcct ctgggctgtg aaagacacta tgcaagctca 500
212 ggataacatc acgagtgtcc ggctgctgca gcaggagggt ctgcagaacg 550
214 tctcggtatg tgagagctgt taccttgtcc acaccctgct ggagttctac 600
216 ttgaaaactg ttttcaaaaa ccaccacaat agaacagttg aagtcaggac 650
218 tctgaagtca ttctctactc tggccaacaa ctttggttctc atcgtgtcac 700
220 aactgcaacc cagtcaagaa aatgagatgt tttccatcag agacagtgc 750
222 cacaggcggg ttctgctatt ccggagagca ttcaaacagt tggacgtaga 800
224 agcagctctg accaaagccc ttgggggaagt ggacattctt ctgacctgga 850
226 tgcagaaatt ctacaagctc tgaatgtcta gaccaggacc tccctccccc 900
228 tggcactggg ttgttcctct tgtcatttca aacagtctcc cttcctatgc 950

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230  tgttcactgg acacttcacg cccttggcca tgggtcccat tcttggccca 1000
232  ggattattgt caaagaagtc attctttaag cagcgccagt gacagtcagg 1050
234  gaaggtgcct ctggatgctg tgaagagtct acagagaaga ttcttgtatt 1100
236  tattacaact ctattttaatt aatgtcagta tttcaactga agttctatct 1150
238  atttgtgaga ctgtaagtta catgaaggca gcagaatatt gtgccccatg 1200
240  cttctttacc cctcacaatc cttgccacag tgtggggcag tggatgggtg 1250
242  cttagtaagt acttaataaa ctgtgggtgct ttttttggcc tgtctttgga 1300
244  ttgttaaaaa acagagaggg atgcttggat gtaaaactga acttcagagc 1350
246  atgaaaatca cactgtcttc tgatatctgc agggacagag cattgggggtg 1400
248  ggggtaaggt gcatctgttt gaaaagtaaa cgataaaatg tggattaaag 1450
250  tgcccagcac aaagcagatc ctcaataaac atttcatttc ccaccacac 1500
252  tcgccagctc accccatcat ccctttccct tggtgccctc cttttttttt 1550
254  taccctagtc attcttccct aatcttccac ttgagtgtca agctgacctt 1600
256  gctgatgggtg acattgcacc tggatgtact atccaatctg tgatgacatt 1650
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260  aaaaaa 1705

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262 <210> SEQ ID NO: 7

263 <211> LENGTH: 206

264 <212> TYPE: PRT

265 <213> ORGANISM: Homo Sapien

267 <400> SEQUENCE: 7

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269      1                      5                      10                      15
271  Pro Phe Cys Pro Pro Leu Leu Ala Thr Ala Ser Gln Met Gln Met
272                      20                      25                      30
274  Val Val Leu Pro Cys Leu Gly Phe Thr Leu Leu Leu Trp Ser Gln
275                      35                      40                      45
277  Val Ser Gly Ala Gln Gly Gln Glu Phe His Phe Gly Pro Cys Gln
278                      50                      55                      60
280  Val Lys Gly Val Val Pro Gln Lys Leu Trp Glu Ala Phe Trp Ala
281                      65                      70                      75
283  Val Lys Asp Thr Met Gln Ala Gln Asp Asn Ile Thr Ser Ala Arg
284                      80                      85                      90
286  Leu Leu Gln Gln Glu Val Leu Gln Asn Val Ser Asp Ala Glu Ser
287                      95                      100                     105
289  Cys Tyr Leu Val His Thr Leu Leu Glu Phe Tyr Leu Lys Thr Val
290                      110                     115                     120
292  Phe Lys Asn His His Asn Arg Thr Val Glu Val Arg Thr Leu Lys
293                      125                     130                     135
295  Ser Phe Ser Thr Leu Ala Asn Asn Phe Val Leu Ile Val Ser Gln
296                      140                     145                     150
298  Leu Gln Pro Ser Gln Glu Asn Glu Met Phe Ser Ile Arg Asp Ser
299                      155                     160                     165
301  Ala His Arg Arg Phe Leu Leu Phe Arg Arg Ala Phe Lys Gln Leu
302                      170                     175                     180
304  Asp Val Glu Ala Ala Leu Thr Lys Ala Leu Gly Glu Val Asp Ile
305                      185                     190                     195
307  Leu Leu Thr Trp Met Gln Lys Phe Tyr Lys Leu
308                      200                     205

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